

Patent Application US/07/807,043

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon, Thierry, Van den Eynde, Beno t
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Felfe & Lynch
- (B) STREET: 805 Third Avenue
- (C) CITY: New York City
- (D) STATE: New York
- (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
- (B) COMPUTER: IBM
- (C) OPERATING SYSTEM: PC-DOS
- (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/807,043
- (B) FILING DATE: 12-DECEMBER-1991
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/764,364
- (B) FILING DATE: 23-SEPTEMBER-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/728,838
- (b) FILING DATE: 9-JULY-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/705,702
- (B) FILING DATE: 23-May-1991
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Hanson, Norman D.
- (B) REGISTRATION NUMBER: 30,946
- (C) REFERENCE/DOCKET NUMBER: LUD 253.3
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (212) 688-9200
- (B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQUENCE ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid

(c) Strandedness: _____

See p. 188

Please insert this field.
It is mandatory for
each nucleic sequence.
(Insert for all 16 sequences)

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54 (D) TOPOLOGY: linear
55 (ii) MOLECULE TYPE: genomic DNA
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
57
58
59
60
61 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
62 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
63 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTCGA AGTCCGCCT ACAGCTCTAG 180
64 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
65 CCCCCCTCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
66 AGAAGTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
67 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
68 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462
69
70
71 (2) INFORMATION FOR SEQUENCE ID NO: 2:
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 675 base pairs
74 (B) TYPE: nucleic acid
75 (D) TOPOLOGY: linear
76 (ii) MOLECULE TYPE: genomic DNA
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
78
79
80 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
81 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
82 5 10 15
83
84 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
85 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
86 20 25 30
87
88 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
89 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
90 35 40 45
91
92 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
93 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
94 50 55 60
95
96 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
97 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
98 65 70 75 80
99
100 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
101 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
102 85 90 95
103
104 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336
105 Asp Asp Glu Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
106 100 105 110

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107
108 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG 384
109 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
110 115 120 125
111
112 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432
113 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
114 130 135 140
115
116 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480
117 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
118 145 150 155 160
119
120 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC 528
121 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
122 165 170 175
123
124 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576
125 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
126 180 185 190
127
128 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG 624
129 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
130 195 200 205
131
132 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672
133 Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
134 210 215 220 225
135
136 TAG 675
137
138 (2) INFORMATION FOR SEQUENCE ID NO: 3:
139 (i) SEQUENCE CHARACTERISTICS:
140 (A) LENGTH: 228 base pairs
141 (B) TYPE: nucleic acid
142 (D) TOPOLOGY: linear
143 (ii) MOLECULE TYPE: genomic DNA
144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
145
146
147
148
149 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
150 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
151 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC 180
152 ATAGGATTAC ACTTGACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228
153
154
155
156 (2) INFORMATION FOR SEQUENCE ID NO: 4:
157 (i) SEQUENCE CHARACTERISTICS:
158 (A) LENGTH: 1365 base pairs
159 (B) TYPE: nucleic acid

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160 (D) TOPOLOGY: linear
161 (ii) MOLECULE TYPE: genomic DNA
162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
163
164
165
166
167 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
168 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
169 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
170 AAGTTTTGCA AGTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
171 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
172 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
173 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG 350
174 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
175 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
176 ACCCTTTGTG CC 462
177 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
178 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
179 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
180 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
181 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
182 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
183 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
184 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
185 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
186 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
187 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
188 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
189 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
190 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
191 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
192 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
193 TAG 1137
194 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
195 TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
196 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
197 CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT 1337
198 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365
199
200
201
202 (2) INFORMATION FOR SEQUENCE ID NO: 5:
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 4698 base pairs
205 (B) TYPE: nucleic acid
206 (D) TOPOLOGY: linear
207 (ii) MOLECULE TYPE: genomic DNA
208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
209
210
211
212 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50

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213	GAAGATCCTG	ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	100
214	CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
215	AAGTTTGTGA	AGTTCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
216	CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
217	CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
218	AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTT	GCTCTCCAG	350
219	CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	400
220	CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
221	ACCCTTTGTG	CC				462
222	ATG TCT GAT	AAC AAG AAA	CCA GAC AAA	GCC CAC AGT	GGC TCA	504
223	GGT GGT GAC	GGT GAT GGG	AAT AGG TGC	AAT TTA TTG	CAC CGG	546
224	TAC TCC CTG	GAA GAA ATT	CTG CCT TAT	CTA GGG TGG	CTG GTC	588
225	TTC GCT GTT	GTC ACA ACA	AGT TTT CTG	GCG CTC CAG	ATG TTC	630
226	ATA GAC GCC	CTT TAT GAG	GAG CAG TAT	GAA AGG GAT	GTG GCC	672
227	TGG ATA GCC	AGG CAA AGC	AAG CGC ATG	TCC TCT GTC	GAT GAG	714
228	GAT GAA GAC	GAT GAG GAT	GAT GAG GAT	GAC TAC TAC	GAC GAC	756
229	GAG GAC GAC	GAC GAC GAT	GCC TTC TAT	GAT GAT GAG	GAT GAT	798
230	GAG GAA GAA	GAA TTG GAG	AAC CTG ATG	GAT GAT GAA	TCA GAA	840
231	GAT GAG GCC	GAA GAA GAG	ATG AGC GTG	GAA ATG GGT	GCC GGA	882
232	GCT GAG GAA	ATG GGT GCT	GGC GCT AAC	TGT GCC T		916
233	GTGAGTAACC	CGTGGTCTTT	ACTCTAGATT	CAGGTGGGGT	GCATTCTTTA	966
234	CTCTTGCCCA	CATCTGTAGT	AAAGACCACA	TTTTGGTTGG	GGGTCATTGC	1016
235	TGGAGCCATT	CCTGGCTCTC	CTGTCCACGC	CTATCCCCGC	TCCTCCCATC	1066
236	CCCCACTCCT	TGCTCCGCTC	TCTTTCCTTT	TCCCACCTTG	CCTCTGGAGC	1116
237	TTCAGTCCAT	CCTGCTCTGC	TCCCTTTCCC	CTTTGCTCTC	CTTGCTCCCC	1166
238	TCCCCCTCGG	CTCAACTTTT	CGTGCCTTCT	GCTCTCTGAT	CCCCACCCTC	1216
239	TTCAGGCTTC	CCCATTTGCT	CCTCTCCCCG	AACCCTCCCC	TTCCCTGTTCC	1266
240	CCTTTTTCGG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316
241	TCACCAGCTT	TGCTCTCCCT	GCTCCCCCTC	CCCTTTTGCA	CCTTTTCTTT	1366
242	TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCCT	1416
243	CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTTG	CATTTTCGGG	1466
244	TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTCCGGTGCT	1516
245	CTCCCTCCC	CATCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566
246	TTGGTTTTTT	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCCTGGAC	1616
247	TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	CAGAAATCTG	CCTGCCTCTG	1666
248	CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
249	GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
250	AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816
251	TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
252	CCTCCCCCTC	TTTGCTCGAC	TTTTAGCAGC	CTTACCTCTC	CCTGCTTTCT	1916
253	GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966
254	AGCTCACCTT	TTTGTTTGTT	TGGTTGTTTG	GTTGTTTGGT	TTGCTTTTTT	2016
255	TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCCTCCCC	TCCGGCTTCC	2066
256	CCTCTGTGTG	CCTTTCCTGT	TCCCTCCCCC	TCGCTGGCTC	CCCCCTCCCT	2116
257	TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
258	CTTTTCTAGA	CTCCCCCTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
259	CCTGACCTCG	CTCCCCCTCC	CCTCCAGCT	CCCCCTCTT	TTCCCACCTC	2266
260	CCTTCTCCA	CCTGTTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316
261	TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
262	GACTTCTCT	CCAGCCGCCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416
263	CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCCT	2466
264	ATGTGTCTCT	CTTCTATCT	ATCCCTTCC	TTCTGTCCCC	TCTCCTCTGT	2516
265	CCATCACCTC	TCTCCTCCCT	TCCCTTTCCT	CTCTCTTCCA	TTTTCTTCCA	2566

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266	CCTGCTTCTT	TACCCTGCCT	CTCCCATTC	CCTCTTACCT	TTATGCCCAT	2616
267	TCCATGTCCC	CTCTCAATC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
268	ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
269	TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTTATG	CCCTCTACTC	2766
270	TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCCTTT	CCACCCTGCC	2816
271	CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
272	ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAA	ATCAGCAGGA	2916
273	AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
274	AAGTGGCTCC	TATAACCTTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
275	CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
276	CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
277	GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
278	TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
279	TCCTTCTACA	GGTGAGAAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTTA	3266
280	GGCTAAAGAT	ACTTGGAAAC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
281	TTGCTAAAT	ATTCTTTCTC	ACATATTCAT	ATTCTCCAG		3355
282	GT GTT CCT	GGC CAT CAT	TTA AGG	AAG AAT GAA	GTG AAG TGT	3396
283	AGG ATG ATT	TAT TTC	TTC CAC	GAC CCT AAT	TTC CTG GTG TCT	3438
284	ATA CCA GTG	AAC CCT AAG	GAA CAA	ATG GAG TGT	AGG TGT GAA	3480
285	AAT GCT GAT	GAA GAG GTT	GCA ATG	GAA GAG GAA	GAA GAA GAA	3522
286	GAG GAG GAG	GAG GAG GAA	GAG GAA	ATG GGA AAC	CCG GAT GGC	3564
287	TTC TCA CCT	TAG				3576
288	GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCTAACA	TATGCCTGTA	3626
289	GCTAAGAGCA	TCTTTTTTAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
290	TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
291	CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
292	GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
293	GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
294	TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
295	TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAATTAT	TATTTTGTCTG	3976
296	TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
297	CTTAAATTTT	CCTTCATCTT	TAATTTTCCT	TAACTTTAGT	TTTTTTTCACT	4076
298	TAGAATTCAA	TTCAAATTCT	TAATTCATC	TTAATTTTTA	GATTTCTTAA	4126
299	AATGTTTTTT	AAAAAAAATG	CAAATCTCAT	TTTTTAAGAGA	TGAAAGCAGA	4176
300	GTAAGTGGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
301	GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
302	CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
303	ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
304	ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
305	AGTCAGGAGT	GTATTCTAAT	AAGTGTGCT	TATCTCTTAT	TTTCTTCTAC	4476
306	AGTTGCAAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTTT	4526
307	TTTTTTCCCC	TTCATTAATT	TTCTAGTTTT	TAGTAATCCA	GAAAATTTGA	4576
308	TTTTGTTCTA	AAGTTCATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
309	GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
310	AATAAAAGTT	TGACTTGCAT	AC			4698

311
312

313 (2) INFORMATION FOR SEQUENCE ID NO: 6:

314 (i) SEQUENCE CHARACTERISTICS:

315 (A) LENGTH: 7 amino acids

316 (B) TYPE: amino acid

317 (D) TOPOLOGY: linear

318 (ii) MOLECULE TYPE: protein

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319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

320
321
322
323
324 Leu Pro Tyr Leu Gly Trp Leu
325 5
326
327
328
329
330
331
332

333 (2) INFORMATION FOR SEQUENCE ID NO: 7:

334 (i) SEQUENCE CHARACTERISTICS:

335 (A) LENGTH: 2418 base pairs

336 (B) TYPE: nucleic acid

337 (D) TOPOLOGY: linear

338 (ii) MOLECULE TYPE: genomic DNA

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

340
341
342
343
344 GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG 50
345 GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC 100
346 TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG 150
347 GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT 200
348 TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT 250
349 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
350 CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT 350
351 CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC 400
352 TTCCTCCTTC AGGTTTTTCAG GGGACAGGCC AATCCAGAGG ACAGGATTCC 450
353 CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG 500
354 TTAGAGTCTC CAAGGTTTCTG TTCTCAGCTG AGGCCTCTCA CACACTCCCT 550
355 CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT 600
356 GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC 650
357 ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG 700
358 GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC 750
359 CCTGGAGGAG GTGCCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC 800
360 AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA 850
361 CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG 900
362 TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT 950
363 TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG 1000
364 GCAGAAATG TGGAGATGT CATCAAAAT TACAAGCACT GTTTTCCTGA 1050
365 GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG 1100
366 TGAAGGAAGC AGACCCCAACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA 1150
367 GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200
368 AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG 1250
369 CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300
370 GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350
371 TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC 1400

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372 CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT 1450
373 ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT 1500
374 TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT 1550
375 CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC 1600
376 ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCCTCGT TGACATGAGG 1650
377 CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTTCCTCAGT AGTAGGTTTC 1700
378 TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT 1750
379 TCAAATGTTT TTTTAAAGG GATGGTTGAA TGAACCTCAG CATCCAAGTT 1800
380 TATGAATGAC AGCAGTCACA CAGTTCGTGT TATATAGTTT AAGGGTAAGA 1850
381 GTCTTGTTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG 1900
382 ATAATAACAG CAGTGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA 1950
383 AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCCTGC 2000
384 CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG 2050
385 GATTTCCCTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG 2100
386 AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC 2150
387 TTTTGGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT 2200
388 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 2250
389 AGGTGGCAAC ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 2300
390 GGGTGTGGGG CTCCGGGTGA GAGTGGTGA GTGTCAATGC CCTGAGCTGG 2350
391 GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT 2400
392 AATGATCTTG SGTGGATCC (2418) 2419 are listed

393
394 (2) INFORMATION FOR SEQUENCE ID NO: 8:
395 (i) SEQUENCE CHARACTERISTICS:
396 (A) LENGTH: 5724 base pairs
397 (B) TYPE: nucleic acid
398 (D) TOPOLOGY: linear
399 (ii) MOLECULE TYPE: genomic DNA
400 (ix) FEATURE:
401 (A) NAME/KEY: MAGE-1 gene
402 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
403
404
405

The computer detected a discrepancy - Please recount the base pairs.

406 CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCAAC TCCCTCCCTT 50
407 TACGCCACCC ATCCAAACAT CTTACGCTC ACCCCAGCC CAAGCCAGGC 100
408 AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCAG 150
409 ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200
410 CGGTCTGAGG GCGGCTTGA GATCGGTGGA GGGAAGCGGG CCCAGCTCTG 250
411 TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
412 AGATAGAGGA CCCCATAA TCCCTTCATG CCAGTCCCTG ACCATCTGGT 350
413 GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA 400
414 CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
415 AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
416 AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550
417 ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCAAT CCAACCCCA 600
418 CCCACATCC CCCACCCAT CCCTCAACCC TGATGCCCAT CCGCCAGCC 650
419 ATTCCACCT CACCCCAACC CCCACCCCA CGCCCACTCC CACCCCAACC 700
420 CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC 750
421 GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG 800
422 AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG 850
423 AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA 900
424 GAGAGCCCCA AATATTCCAG CCCCGCCCTT GCTGCCAGCC CTGGCCACC 950

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425	CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
426	CCTTGAGAGA	CACCAGGTTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
427	TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
428	GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
429	ACTCCAATCC	CCACTCCCAC	CCCATTCGCA	TTCCCATTCC	CCACCCAACC	1200
430	CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
431	CCTGACCACC	ACCCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
432	TCACCCTCAC	TGCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
433	CCCATCGCCT	CCCCCATTTCT	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
434	CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
435	AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
436	ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
437	CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
438	ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
439	GTCTCAGCTG	GACCACCCCC	CGTCCCCTCC	CACTGCCACT	TAACCCACAG	1700
440	GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
441	GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
442	ACCTTGGGAG	GGAACTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
443	CACCGGCACC	CCACTCACAT	TCCCATACCT	ACCCCTTACC	CCCAACCTCA	1900
444	TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
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447	GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
448	ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
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451	GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
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466	ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
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475	GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3550
476	GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3600
477	TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3650

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490 GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC 4224
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523 ATTGTAATGA TCTTGGGTGG ATCC 5724
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528 (2) INFORMATION FOR SEQUENCE ID NO: 9:

529 (i) SEQUENCE CHARACTERISTICS:

530 (A) LENGTH: 4157 base pairs

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531 (B) TYPE: nucleic acid
532 (D) TOPOLOGY: linear
533 (ii) MOLECULE TYPE: genomic DNA
534 (ix) FEATURE:
535 (A) NAME/KEY: MAGE-2 gene
536 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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539
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543 GAGGGAAGCA GGCGCAGGCT CCGTGAGGAG GCAAGGTAAG ACGCCGAGGG 200
544 AGGACTGAGG CGGGCCTCAC CCCAGACAGA GGGCCCCCAA TTAATCCAGC 250
545 GCTGCCTCTG CTGCCGGGCC TGGACCACCC TGCAGGGGAA GACTTCTCAG 300
546 GCTCAGTCGC CACCACCTCA CCCC GCCACC CCCC GCCGCT TTAACCGCAG 350
547 GGA ACTCTGG CGTAAGAGCT TTGTGTGACC AGGGCAGGGC TGGTTAGAAG 400
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583 TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC CTCAGGTCAC 2200

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597	TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT	2849
598	GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT	2891
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605	GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG	3185
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620	GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG	3842
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625	TGCTTCTTTG AGAATGCAAA AGAAATTAAT TCTGAATAAA TTCTTCCTGT	4092
626	TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC	4142
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633	(2) INFORMATION FOR SEQUENCE ID NO: 10:	
634	(i) SEQUENCE CHARACTERISTICS:	
635	(A) LENGTH: 662 base pairs	
636	(B) TYPE: nucleic acid	

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637 (D) TOPOLOGY: linear
638 (ii) MOLECULE TYPE: genomic DNA
639 (ix) FEATURE:
640 (A) NAME/KEY: MAGE-21 gene
641 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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654 GAGGGTAACC CCCCCGACC CCCACCACCA TTCCCATCCC CCAACACCAA 500
655 CCCCACCCCC ATCCCCAAC ACCAAACCCA CCACCATCGC TCAAACATCA 550
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668 (2) INFORMATION FOR SEQUENCE ID NO: 11:
669 (i) SEQUENCE CHARACTERISTICS:
670 (A) LENGTH: 1640 base pairs
671 (B) TYPE: nucleic acid
672 (D) TOPOLOGY: linear
673 (ii) MOLECULE TYPE: cDNA to mRNA
674 (ix) FEATURE:
675 (A) NAME/KEY: cDNA MAGE-3
676 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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683 GTTGCCCTGA CCAGAGTCAT C 171
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687 TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 339
688 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381
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696	GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
697	GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
698	CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
699	AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
700	CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
701	TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
702	GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
703	GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
704	ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
705	GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
706	TTG AGA GAG GGG GAA GAG TGA	1116
707	GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
708	GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCCTCC TGTGACGTGA	1216
709	GGCCCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	1266
710	TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG	1316
711	TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
712	GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG	1416
713	TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA	1466
714	TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC	1516
715	GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	1566
716	ATTCTTGCCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA	1616
717	ACCAGGATTT CCTTGACTTC TTTG	1640

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722 (2) INFORMATION FOR SEQUENCE ID NO: 12:

723 (i) SEQUENCE CHARACTERISTICS:

724 (A) LENGTH: 943 base pairs

725 (B) TYPE: nucleic acid

726 (D) TOPOLOGY: linear

727 (ii) MOLECULE TYPE: genomic DNA

728 (ix) FEATURE:

729 (A) NAME/KEY: MAGE-31 gene

730 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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734	GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT	50
735	CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG	100
736	GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG	150
737	AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA	200
738	GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC	250
739	CTGCCCCAGA ACACATGGAG TCCAGAGCGC CTGGCCTCAC CCTCAATACT	300
740	TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC	350
741	CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC	400
742	AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG	450

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743	TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC	500
744	TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCACA	550
745	CTCCCGCCTG TTGCCCTGAC CAGAGTCATC	580
746	ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	622
747	GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG	664
748	CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	706
749	TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	748
750	GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	790
751	CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	832
752	GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	874
753	CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG	916
754	GTG GCC AAG TTG GTT CAT TTT CTG CTC	943

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759 (2) INFORMATION FOR SEQUENCE ID NO: 13:

760 (i) SEQUENCE CHARACTERISTICS:

761 (A) LENGTH: 1067 base pairs

762 (B) TYPE: nucleic acid

763 (D) TOPOLOGY: linear

764 (ii) MOLECULE TYPE: cDNA to mRNA

765 (ix) FEATURE:

766 (A) NAME/KEY: cDNA MAGE-4

767 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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771	GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA	39
772	GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG	81
773	CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA	123
774	ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT	165
775	GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT	207
776	GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC	249
777	ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG	291
778	GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC	333
779	GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG	375
780	GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT	417
781	GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC	459
782	ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG	501
783	GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	543
784	CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	585
785	CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	627
786	TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	669
787	TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG	719
788	TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	769
789	GCCCATCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG	819
790	GTTTCTATTT TGTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA	869
791	ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA	919
792	AGTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT	969
793	AAGAGTCTTG TTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT	1019
794	TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC	1067

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797 (2) INFORMATION FOR SEQUENCE ID NO: 14:

798 (i) SEQUENCE CHARACTERISTICS:

799 (A) LENGTH: 226 base pairs

800 (B) TYPE: nucleic acid

801 (D) TOPOLOGY: linear

802 (ii) MOLECULE TYPE: genomic DNA

803 (ix) FEATURE:

804 (A) NAME/KEY: MAGE-5 gene

805 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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809 AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT 50

810 AAGCCTTTGT TAGAGCCTCC AAGGTTCAAGT TTTTAGCTGA GGCTTCTCAC 100

811 ATGCTCCCTC TCTCTCCAGG CCAAGTGGGTC TCCATTGCCC AGCTCCTGCC 150

812 CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 184

813 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 226

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815 (2) INFORMATION FOR SEQUENCE ID NO: 15:

816 (i) SEQUENCE CHARACTERISTICS:

817 (A) LENGTH: 225 base pairs

818 (B) TYPE: nucleic acid

819 (D) TOPOLOGY: linear

820 (ii) MOLECULE TYPE: cDNA

821 (ix) FEATURE:

822 (A) NAME/KEY: MAGE-6 gene

823 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

824

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827 TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG 42

828 CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC 84

829 GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC 126

830 GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC 168

831 TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC 210

832 TGT GCC CCT GAG GAG 225

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838 (2) INFORMATION FOR SEQUENCE ID NO: 16:

839 (i) SEQUENCE CHARACTERISTICS:

840 (A) LENGTH: 166 base pairs

841 (B) TYPE: nucleic acid

842 (D) TOPOLOGY: linear

843 (ii) MOLECULE TYPE: genomic DNA

844 (ix) FEATURE:

845 (A) NAME/KEY: MAGE-7 gene

846 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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849
850 ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG 42
851 TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC 84
852 CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC 126
853 TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A 166
854

LINE ERROR

ORIGINAL TEXT

24	Wrong application Serial Number
34	Response Exceeds Line Limitations
56	Wrong Or Missing Strandedness Value
77	Wrong Or Missing Strandedness Value
144	Wrong Or Missing Strandedness Value
162	Wrong Or Missing Strandedness Value
208	Wrong Or Missing Strandedness Value
339	Wrong Or Missing Strandedness Value
339	Entered and Calc. Seq. Length differ
402	Wrong Or Missing Strandedness Value
402	Entered and Calc. Seq. Length differ
536	Wrong Or Missing Strandedness Value
641	Wrong Or Missing Strandedness Value
676	Wrong Or Missing Strandedness Value
730	Wrong Or Missing Strandedness Value
767	Wrong Or Missing Strandedness Value
805	Wrong Or Missing Strandedness Value
823	Wrong Or Missing Strandedness Value
846	Wrong Or Missing Strandedness Value

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PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/807,043

DATE: 07/18/92
TIME: 11:55:30

MANDATORY IDENTIFIER THAT WAS NOT FOUND

COUNTRY
STRANDEDNESS

LINE ORIGINAL TEXT

CORRECTED TEXT

3 (i) APPLICANTS: Boon, Thierry, Van den
50 (2) INFORMATION FOR SEQUENCE ID NO: 1:
71 (2) INFORMATION FOR SEQUENCE ID NO: 2:
138 (2) INFORMATION FOR SEQUENCE ID NO: 3:
156 (2) INFORMATION FOR SEQUENCE ID NO: 4:
202 (2) INFORMATION FOR SEQUENCE ID NO: 5:
313 (2) INFORMATION FOR SEQUENCE ID NO: 6:
333 (2) INFORMATION FOR SEQUENCE ID NO: 7:
394 (2) INFORMATION FOR SEQUENCE ID NO: 8:
528 (2) INFORMATION FOR SEQUENCE ID NO: 9:
633 (2) INFORMATION FOR SEQUENCE ID NO: 10:
668 (2) INFORMATION FOR SEQUENCE ID NO: 11:
722 (2) INFORMATION FOR SEQUENCE ID NO: 12:
759 (2) INFORMATION FOR SEQUENCE ID NO: 13:
797 (2) INFORMATION FOR SEQUENCE ID NO: 14:
815 (2) INFORMATION FOR SEQUENCE ID NO: 15:
838 (2) INFORMATION FOR SEQUENCE ID NO: 16:

(i) APPLICANT: Boon, Thierry, Van den E
(2) INFORMATION FOR SEQ ID NO: 1:
(2) INFORMATION FOR SEQ ID NO: 2:
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(2) INFORMATION FOR SEQ ID NO: 4:
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(2) INFORMATION FOR SEQ ID NO: 13:
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(2) INFORMATION FOR SEQ ID NO: 15:
(2) INFORMATION FOR SEQ ID NO: 16: